Claims

1. Primers with a length of 17 to 25 nucleotides, whose sequences are identical to a sequence as shown in SEQ ID No. 1-4, or whose sequences represent part-sequences of one of the sequences as shown in SEQ ID No. 1-4, or in which a sequence as shown in SEQ ID No. 1-4 forms a continuous part-sequence of the primer.

2. A multiplex amplification reaction for detecting clinically relevant EHEC infections, in which both stxA1 and stxA2 sequences of both human-pathogenic and swine-pathogenic stx2 isoforms are amplified, characterized in that one, more than one or all of the primers as claimed in claim 1 are used.

3. The use of primers as claimed in claim 1 for detecting an EHEC infection.

4. A method as claimed in claim 2 or 3, characterized in that the product of the amplification reaction is additionally detected by hybridization.

5. The method as claimed in claim 4, characterized in that a hybridization probe has a sequence which is identical or complementary to the region which codes for the enzymatically active site of the polypeptide chain encoded by the stxA1 gene or the stxA2 gene.

6. The method as claimed in claim 2-5, characterized in that the amplification product is detected with the aid of fluorescence detection.

7. The method as claimed in claim 6, characterized in that the amplification product is detected with the aid of a compound which fluoresces on binding to double-stranded DNA.

8. The method as claimed in claim 4-6, characterized in that the amplification product is detected with the aid of fluorescence resonance energy transfer.

9. The method as claimed in claim 8, in which there is use of an internal standard which differs from the stxA1 or the stxA2 sequence only in one or two point mutations, characterized in that amplified target DNA and internal standard are distinguished from one another by means of a melting curve analysis.

10. The method as claimed in claim 8 or 9, characterized in that human-pathogenic stxA2 and swine-pathogenic $stxA2_e$ are distinguished by means of a melting curve analysis.

11. Hybridization probes having sequences or part-sequences as shown in SEQ ID No. 5-8.

12. The method as claimed in claim 9 or 10, characterized in that hybridization probes with sequences as given in claim 11 are used.

13. Use of hybridization probes as claimed in claim 11 for determining melting curves.

14. A kit for detecting clinically relevant EHEC infections, comprising primers as claimed in claim 1.

15. A kit as claimed in claim 14, comprising hybridization probes.

16. A kit as claimed in claim 14 or 15, comprising reagents for amplifying additional pathogenicity factors.